



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,069A

DATE: 10/12/2004

TIME: 13:50:27

Input Set : A:\9151-6.ST25.txt

Output Set: N:\CRF4\10122004\I823069A.raw

3 <110> APPLICANT: Wheeler, Kenneth
4 Mach, Robert
5 Childers, Steven
6 Shelness, Gregory
7 Wang, Li-Ming
9 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPL
VARIANT
10 OF THE SIGMA-1 RECEPTOR
12 <130> FILE REFERENCE: 9151-6
14 <140> CURRENT APPLICATION NUMBER: US 09/823,069A
15 <141> CURRENT FILING DATE: 2001-03-30
17 <150> PRIOR APPLICATION NUMBER: US 60/193,694
18 <151> PRIOR FILING DATE: 2000-03-31
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 579
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(579)
34 <400> SEQUENCE: 1
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37 1 5 10 15
39 gct gtc gca gcg gtg ctg acc cag gtc gtc tgg ctc tgg ctg ggt acg 96
40 Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr
41 20 25 30
43 cag agc ttc gtc ttc cag cgc gaa gag ata gcg cag ttg gcg cgg cag 144
44 Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
45 35 40 45
47 tac gct ggg ctg gac cac gag ctg gcc ttc tct cgt ctg atc gtg gag 192
48 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
49 50 55 60
51 ctg cgg cgg ctg cac cca ggc cac gtg ctg ccc gac gag gag ctg cag 240
52 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
53 65 70 75 80
55 tgg gtg ttc gtg aat gcg ggt ggc tgg atg ggc gcc atg tgc ctt ctg 288
56 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu
57 85 90 95
59 cac gcc tcg ctg tcc gag tat gtg ctg ctc ttc ggc acc gcc ttg ggc 336
60 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
61 100 105 110

ENTERED

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63 tcc cgc ggc cac tcg ggg gag acg gta gta cac ggg cct ggt gag gca      384
64 Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
65      115      120      125
67 aca gct gtg gag tgg ggg cca aac aca tgg atg gtg gag tac ggc cgg      432
68 Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
69      130      135      140
71 ggc gtc atc cca tcc acc ctg gcc ttc gcg ctg gcc gac act gtc ttc      480
72 Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe
73 145      150      155      160
75 agc acc cag gac ttc ctc acc ctc ttc tat act ctt cgc tcc tat gct      528
76 Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala
77      165      170      175
79 cgg ggc ctc cgg ctt gag ctc acc acc tac ctc ttt ggc cag gac cct      576
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88 <212> TYPE: PRT
89 <213> ORGANISM: Homo sapiens
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98      20      25      30
101 Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
102      35      40      45
105 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
106      50      55      60
109 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
110 65      70      75      80
113 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu
114      85      90      95
117 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
118      100      105      110
121 Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
122      115      120      125
125 Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
126      130      135      140
129 Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe
130 145      150      155      160
133 Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala
134      165      170      175
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138      180      185      190
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 579
143 <212> TYPE: DNA
144 <213> ORGANISM: Mus musculus
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147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)..(579)
151 <400> SEQUENCE: 3

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153	Met	Pro	Trp	Ala	Ala	Gly	Arg	Arg	Trp	Ala	Trp	Ile	Thr	Leu	Ile	Leu	
154	1				5					10					15		
156	act	att	atc	gca	gtg	ctg	atc	cag	gcc	gcc	tgg	ttg	tgg	ctg	ggc	act	96
157	Thr	Ile	Ile	Ala	Val	Leu	Ile	Gln	Ala	Ala	Trp	Leu	Trp	Leu	Gly	Thr	
158					20				25					30			
160	caa	aac	ttc	gtc	ttc	tct	aga	gaa	gaa	ata	gcg	cag	ctt	gct	cga	cag	144
161	Gln	Asn	Phe	Val	Phe	Ser	Arg	Glu	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Gln	
162				35				40				45					
164	tat	gcg	ggg	ctg	gac	cat	gag	ctt	gcc	ttc	tct	cgg	ctg	atc	gtg	gag	192
165	Tyr	Ala	Gly	Leu	Asp	His	Glu	Leu	Ala	Phe	Ser	Arg	Leu	Ile	Val	Glu	
166		50					55					60					
168	ctg	cgg	agg	ctg	cac	cca	ggc	cac	gtg	ctg	ccg	gat	gag	gag	ctg	cag	240
169	Leu	Arg	Arg	Leu	His	Pro	Gly	His	Val	Leu	Pro	Asp	Glu	Glu	Leu	Gln	
170	65					70				75					80		
172	tgg	gta	ttt	gtg	aac	gcg	ggc	ggc	tgg	atg	ggc	gcc	atg	tgt	att	ctg	288
173	Trp	Val	Phe	Val	Asn	Ala	Gly	Gly	Trp	Met	Gly	Ala	Met	Cys	Ile	Leu	
174					85				90					95			
176	cac	gcc	tcg	ctg	tct	gag	tac	gtg	ctg	ctc	ttc	ggc	acc	gcc	ctg	ggc	336
177	His	Ala	Ser	Leu	Ser	Glu	Tyr	Val	Leu	Leu	Phe	Gly	Thr	Ala	Leu	Gly	
178				100					105					110			
180	tcc	cat	ggc	cat	tcg	gga	gag	aca	gtt	gta	cac	ggg	cct	gga	gaa	gca	384
181	Ser	His	Gly	His	Ser	Gly	Glu	Thr	Val	Val	His	Gly	Pro	Gly	Glu	Ala	
182				115				120					125				
184	acg	gct	ctg	gag	tgg	gga	cca	aac	acg	tgg	atg	gtg	gag	tac	ggc	cgg	432
185	Thr	Ala	Leu	Glu	Trp	Gly	Pro	Asn	Thr	Trp	Met	Val	Glu	Tyr	Gly	Arg	
186		130					135					140					
188	ggt	gtt	att	ccg	tct	acc	ctg	ttc	ttt	gca	cta	gcc	gac	acc	ttc	ttc	480
189	Gly	Val	Ile	Pro	Ser	Thr	Leu	Phe	Phe	Ala	Leu	Ala	Asp	Thr	Phe	Phe	
190	145					150				155					160		
192	ggc	acc	cag	gac	tac	ctc	aca	ctc	ttc	tat	acc	ctt	cgg	gcc	tat	gcc	528
193	Gly	Thr	Gln	Asp	Tyr	Leu	Thr	Leu	Phe	Tyr	Thr	Leu	Arg	Ala	Tyr	Ala	
194				165						170				175			
196	cgg	ggc	ctc	cgg	ctt	gag	ctt	acc	acc	tac	ctc	ttt	ggc	caa	gac	tcc	576
197	Arg	Gly	Leu	Arg	Leu	Glu	Leu	Thr	Thr	Tyr	Leu	Phe	Gly	Gln	Asp	Ser	
198				180					185					190			
200	tga																579
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210	Met	Pro	Trp	Ala	Ala	Gly	Arg	Arg	Trp	Ala	Trp	Ile	Thr	Leu	Ile	Leu	
211	1				5					10				15			
214	Thr	Ile	Ile	Ala	Val	Leu	Ile	Gln	Ala	Ala	Trp	Leu	Trp	Leu	Gly	Thr	

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215          20          25          30
218 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
219          35          40          45
222 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
223          50          55          60
226 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
227 65          70          75          80
230 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu
231          85          90          95
234 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
235          100         105         110
238 Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala
239          115         120         125
242 Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg
243          130         135         140
246 Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe
247 145         150         155         160
250 Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala
251          165         170         175
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255          180         185         190
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259 <211> LENGTH: 31
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Synthetic oligonucleotide primer
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285 <213> ORGANISM: Homo sapiens
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294          20          25          30
297 Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
298          35          40          45
301 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu

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```
302      50      55      60
305 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
306 65      70      75      80
309 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu
310      85      90      95
313 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
314      100      105      110
317 Ser Arg Gly His Ser Gly Arg Tyr Trp Ala Glu Ile Ser Asp Thr Ile
318      115      120      125
321 Ile Ser Gly Thr Phe His Gln Trp Arg Glu Gly Thr Thr Lys Ser Glu
322      130      135      140
325 Val Phe Tyr Pro Gly Glu Thr Val Val His Gly Pro Gly Glu Ala Thr
326 145      150      155      160
329 Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg Gly
330      165      170      175
333 Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe Ser
334      180      185      190
337 Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala Arg
338      195      200      205
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348 <213> ORGANISM: Mus musculus
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357      20      25      30
360 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln
361      35      40      45
364 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu
365      50      55      60
368 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln
369 65      70      75      80
372 Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Ile Leu
373      85      90      95
376 His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly
377      100      105      110
380 Ser His Gly His Ser Gly Arg Tyr Trp Ala Glu Ile Ser Asp Thr Ile
381      115      120      125
384 Ile Ser Gly Thr Phe His Gln Trp Lys Glu Gly Thr Thr Lys Ser Glu
385      130      135      140
388 Val Phe Tyr Pro Gly Glu Thr Val Val His Gly Pro Gly Glu Ala Thr
389 145      150      155      160
392 Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg Gly
393      165      170      175
396 Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe Gly
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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6

VERIFICATION SUMMARY

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